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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=6; day=19; hr=15; min=15; sec=19; ms=314;]

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Reviewer Comments:

<210> 23

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> PP2A motif

<400> 23

Gly Asp Xaa His Gln Gly Gln

1

5

A mandatory feature is required to cover every "Xaa" used in a sequence. SEQ ID # 23 and 24 does not have a feature to cover the "Xaa" at positions 3, and 3,5. Please check for similar errors and make all necessary changes.

Application No: 10590551 Version No: 2.0

Input Set:

Output Set:

Started: 2009-06-03 19:00:30.722
Finished: 2009-06-03 19:00:33.549
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 827 ms
Total Warnings: 15
Total Errors: 5
No. of SeqIDs Defined: 26
Actual SeqID Count: 26

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
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W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
E 341	'Xaa' position not defined SEQID (23) POS (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
E 341	'Xaa' position not defined SEQID (24) POS (3)
E 341	'Xaa' position not defined SEQID (24) POS (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)

SEQUENCE LISTING

<110> Genomine, Inc.
POSTECH FOUNDATION

<120> Novel Phytochrome-interacting protein and a use thereof

<130> OP05-1002

<140> 10590551

<141> 2009-06-03

<150> KR10-2004-0013663

<151> 2004-02-27

<160> 26

<170> KopatentIn 1.71

<210> 1

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 1

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<210> 2

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> PCR primer

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ctcgagctac ttgtttgctg cagcgagttc

30

<210> 3

<211> 1455

<212> DNA

<213> Arabidopsis thaliana

<400> 3

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120

gaactcaaca gcaacaacgc tgtgtattgg gcaaatacgtg catttgctca cacaaaaactg

180

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ctaaaggaat gtgagaaagc agtgatgaaa ctcaaatttg aagaagcaat ctctgtgcca	420
gtatctgaaa ggcgttcagt agctgagtc attgacttcc atacaataga ggttgagcca	480
caatattctg gtgctagaat tgagggagag gaagttacct tagattttgt gaaaacgatg	540
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gagcttaattg gcctcccttc ggaggagaac ccatacctat ttaatggcga ctttgtggac	780
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cttttcagtg ttgacggcgt gaaactctca gacatcagag ccattgacag attctgtgag	1080
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<210> 4
 <211> 484
 <212> PRT
 <213> Arabidopsis thaliana

<400> 4
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 Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
 20 25 30

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Tyr	Trp	Ala	Asn	Arg	Ala	Phe	Ala	His	Thr	Lys	Leu	Glu	Glu	Tyr	Gly	50	55	60
Ser	Ala	Ile	Gln	Asp	Ala	Ser	Lys	Ala	Ile	Glu	Val	Asp	Ser	Arg	Tyr	65	70	75
Ser	Lys	Gly	Tyr	Tyr	Arg	Arg	Gly	Ala	Ala	Tyr	Leu	Ala	Met	Gly	Lys	85	90	95
Phe	Lys	Asp	Ala	Leu	Lys	Asp	Phe	Gln	Gln	Val	Lys	Arg	Leu	Ser	Pro	100	105	110
Asn	Asp	Pro	Asp	Ala	Thr	Arg	Lys	Leu	Lys	Glu	Cys	Glu	Lys	Ala	Val	115	120	125
Met	Lys	Leu	Lys	Phe	Glu	Glu	Ala	Ile	Ser	Val	Pro	Val	Ser	Glu	Arg	130	135	140
Arg	Ser	Val	Ala	Glu	Ser	Ile	Asp	Phe	His	Thr	Ile	Glu	Val	Glu	Pro	145	150	155
Gln	Tyr	Ser	Gly	Ala	Arg	Ile	Glu	Gly	Glu	Glu	Val	Thr	Leu	Asp	Phe	165	170	175
Val	Lys	Thr	Met	Met	Glu	Asp	Phe	Lys	Asn	Gln	Lys	Thr	Leu	His	Lys	180	185	190
Arg	Tyr	Ala	Tyr	Gln	Ile	Val	Leu	Gln	Thr	Arg	Gln	Ile	Leu	Leu	Ala	195	200	205
Leu	Pro	Ser	Leu	Val	Asp	Ile	Ser	Val	Pro	His	Gly	Lys	His	Ile	Thr	210	215	220
Val	Cys	Gly	Asp	Val	His	Gly	Gln	Phe	Tyr	Asp	Leu	Leu	Asn	Ile	Phe	225	230	235
Glu	Leu	Asn	Gly	Leu	Pro	Ser	Glu	Glu	Asn	Pro	Tyr	Leu	Phe	Asn	Gly	245	250	255
Asp	Phe	Val	Asp	Arg	Gly	Ser	Phe	Ser	Val	Glu	Ile	Ile	Leu	Thr	Leu	260	265	270
Phe	Ala	Phe	Lys	Cys	Met	Cys	Pro	Ser	Ser	Ile	Tyr	Leu	Ala	Arg	Gly	275	280	285
Asn	His	Glu	Ser	Lys	Ser	Met	Asn	Lys	Ile	Tyr	Gly	Phe	Glu	Gly	Glu	290	295	300
Val	Arg	Ser	Lys	Leu	Ser	Glu	Lys	Phe	Val	Asp	Leu	Phe	Ala	Glu	Val	305	310	315
Phe	Cys	Tyr	Leu	Pro	Leu	Ala	His	Val	Ile	Asn	Gly	Lys	Val	Phe	Val	325	330	335

Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
 340 345 350
 Arg Ala Ile Asp Arg Phe Cys Glu Pro Pro Glu Glu Gly Leu Met Cys
 355 360 365
 Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
 370 375 380
 Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
 385 390 395 400
 Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
 405 410 415
 Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
 420 425 430
 Ser Ala Pro Asn Tyr Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile
 435 440 445
 Arg Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala
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 465 470 475 480
 Arg Met Phe Asn

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<220>
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24

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 <212> DNA
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<220>
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<400> 6
 ctcgagttag ttgaacatcc tgag

24

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<400> 7
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28

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ggatccatgc cagtatctga aaggcgt 27

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<210> 13
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<400> 13
ttagttgaac atcctgagaa agtt 24

<210> 14
<211> 347
<212> PRT
<213> Arabidopsis thaliana

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35 40 45
Asn Gln Lys Thr Leu His Lys Arg Tyr Ala Tyr Gln Ile Val Leu Gln
50 55 60
Thr Arg Gln Ile Leu Leu Ala Leu Pro Ser Leu Val Asp Ile Ser Val
65 70 75 80
Pro His Gly Lys His Ile Thr Val Cys Gly Asp Val His Gly Gln Phe

85										90					95				
Tyr	Asp	Leu	Leu	Asn	Ile	Phe	Glu	Leu	Asn	Gly	Leu	Pro	Ser	Glu	Glu				
			100							105				110					
Asn	Pro	Tyr	Leu	Phe	Asn	Gly	Asp	Phe	Val	Asp	Arg	Gly	Ser	Phe	Ser				
		115					120					125							
Val	Glu	Ile	Ile	Leu	Thr	Leu	Phe	Ala	Phe	Lys	Cys	Met	Cys	Pro	Ser				
		130					135					140							
Ser	Ile	Tyr	Leu	Ala	Arg	Gly	Asn	His	Glu	Ser	Lys	Ser	Met	Asn	Lys				
145					150					155					160				
Ile	Tyr	Gly	Phe	Glu	Gly	Glu	Val	Arg	Ser	Lys	Leu	Ser	Glu	Lys	Phe				
				165					170					175					
Val	Asp	Leu	Phe	Ala	Glu	Val	Phe	Cys	Tyr	Leu	Pro	Leu	Ala	His	Val				
		180						185					190						
Ile	Asn	Gly	Lys	Val	Phe	Val	Val	His	Gly	Gly	Leu	Phe	Ser	Val	Asp				
		195						200				205							
Gly	Val	Lys	Leu	Ser	Asp	Ile	Arg	Ala	Ile	Asp	Arg	Phe	Cys	Glu	Pro				
		210					215				220								
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225					230					235					240				
Leu	Pro	Gly	Arg	Gly	Pro	Ser	Lys	Arg	Gly	Val	Gly	Leu	Ser	Phe	Gly				
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Gly	Asp	Val	Thr	Lys	Arg	Phe	Leu	Gln	Asp	Asn	Asn	Leu	Asp	Leu	Leu				
		260						265					270						
Val	Arg	Ser	His	Glu	Val	Lys	Asp	Glu	Gly	Tyr	Glu	Val	Glu	His	Asp				
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Gly	Lys	Leu	Ile	Thr	Val	Phe	Ser	Ala	Pro	Asn	Tyr	Cys	Asp	Gln	Met				
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Gly	Asn	Lys	Gly	Ala	Phe	Ile	Arg	Phe	Glu	Ala	Pro	Asp	Met	Lys	Pro				
305					310					315					320				
Asn	Ile	Val	Thr	Phe	Ser	Ala	Val	Pro	His	Pro	Asp	Val	Lys	Pro	Met				
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 <212> DNA
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acgatgatgg aggatttttaa gaacccaaaaa acattgcata aacggtatgc ctatcaaatac      180
gtcttacaga ctaggcaaata cttgctagca ctgccttctc ttgttgatat aagtgttcca      240
catggcaaac atatcactgt ttgcggtgac gttcatggtc agttctacga tcttctcaat      300
atctttgagc ttaatggcct cccttcggag gagaacccat acctatttaa tggcgacttt      360
gtggacagag gctcattctc cgttgagatc atcctcactt tgtttgcttt caagtgcattg      420
tgcccatcat ccatatatct agccagagga aaccatgaaa gcaagagcat gaacaaaatt      480
tatggttttg agggtgaggt tcgggtccaag ttgagtgaaa aattcgtgga tctctttgct      540
gaagttttct gttacctccc gttggctcat gttataaatg ggaaggctct cgtgggtacat      600
ggaggtcttt tcagtgttga cggcgtgaaa ctctcagaca tcagagccat tgacagattc      660
tgtgagccac cagaggaagg actaatgtgt gaactattgt ggagtgatec tcaacctctc      720
cctggaagag gcccaagcaa gcgaggagtt ggtctatcat ttggtggaga tgtgacaaaag      780
aggtttttgc aagataacaa tttagatttg ttggtccggt cacatgaagt aaaagatgaa      840
ggttatgagg ttgaacatga cggtaaaactc ataactgtct tctctgcgcc aaattactgt      900
gatcagatgg gtaataaggg agccttcatt cgttttgaag ctctgatata gaagccaaac      960
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<211>      479
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<213>      Homo sapiens

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<222>      (1)
<223>      PAPP5

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Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
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Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
      35              40              45

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Tyr	Trp	Ala	Asn	Arg	Ala	Phe	Ala	His	Thr	Lys	Leu	Glu	Glu	Tyr	Gly	50	55	60	
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Ser	Lys	Gly	Tyr	Tyr	Arg	Arg	Gly	Ala	Ala	Tyr	Leu	Ala	Met	Gly	Lys	85	90	95	
Glu	Lys	Asp	Ala	Leu	Lys	Asp	Phe	Gln	Gln	Val	Lys	Gly	Leu	Ser	Pro	100	105	110	
Asn	Asp	Pro	Asp	Ala	Thr	Arg	Lys	Leu	Lys	Glu	Cys	Glu	Lys	Ala	Val	115	120	125	
Met	Lys	Leu	Lys	Phe	Glu	Glu	Ala	Ile	Ser	Val	Pro	Val	Ser	Glu	Arg	130	135	140	
Arg	Ser	Val	Ala	Glu	Ser	Ile	Asp	Phe	His	Thr	Ile	Glu	Val	Glu	Pro	145	150	155	160
Gln	Tyr	Ser	Gly	Ala	Arg	Ile	Glu	Gly	Glu	Glu	Val	Thr	Leu	Asp	Phe	165	170	175	
Val	Lys	Thr	Met	Met	Glu	Asp	Phe	Lys	Asn	Gln	Lys	Thr	Leu	His	Lys	180	185	190	
Arg	Tyr	Ala	Tyr	Gln	Ile	Val	Leu	Gln	Thr	Arg	Gln	Ile	Leu	Leu	Ala	195	200	205	
Leu	Pro	Ser	Leu	Val	Asp	Ile	Ser	Val	Pro	His	Gly	Lys	His	Ile	Thr	210	215	220	
Val	Cys	Gly	Asp	Val	His	Gly	Gln	Phe	Tyr	Asp	Leu	Leu	Asn	Ile	Phe	225	230	235	240
Glu	Asp	Asn	Gly	Leu	Pro	Ser	Glu	Glu	Asn	Pro	Tyr	Leu	Phe	Asn	Gly	245	250	255	
Asp	Phe	Val	Asp	Arg	Gly	Ser	Phe	Ser	Val	Glu	Ile	Ile	Leu	Thr	Leu	260	265	270	
Phe	Ala	Glu	Lys	Cys	Met	Cys	Pro	Ser	Ser	Ile	Tyr	Leu	Ala	Arg	Gly	275	280	285	
Asn	His	Glu	Ser	Lys	Ser	Met	Asn	Lys	Ile	Tyr	Gly	Phe	Glu	Gly	Glu	290	295	300	
Val	Arg	Ser	Lys	Leu	Ser	Glu	Lys	Phe	Val	Asp	Leu	Phe	Ala	Glu	Val	305	310	315	320
Phe	Cys	Tyr	Leu	Pro	Leu	Ala	His	Val	Ile	Asn	Gly	Lys	Val	Phe	Val	325	330	335	
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Arg Ala Ile Asp Arg Phe Cys Glu Pro Phe Glu Glu Gly Leu Met Cys
 355 360 365

Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
 370 375 380

Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
 385 390 395 400

Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
 405 410 415

Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
 420 425 430

Ser Ala Pro Asn Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile Arg
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Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala Val
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Pro His Pro Met Ala Tyr Ala Asn Asn Phe Ile Arg Met Phe Asn
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<210> 17
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 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)
 <223> PP5

<400> 17

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Gly Ala Leu Lys Arg Ala Glu Glu Leu Lys Thr Gln Ala Asn Asp Tyr
 20 25 30

Phe Lys Ala Lys Asp Tyr Glu Asn Ala Ile Lys Phe Tyr Ser Gln Ala
 35 40 45

Ile Glu Leu Asn Pro Ser Asn Ala Ile Tyr Tyr Gly Asn Arg Ser Leu
 50 55 60

Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr Ala Leu Gly Asp Ala Thr
 65 70 75 80

Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile Lys Gly Tyr Tyr Arg Arg
 85 90 95

Ala Ala Ser Asn Met Ala Leu Gly Lys Phe Arg Ala Ala Leu Arg Asp

100

105

110

Tyr Glu Thr Val Val Lys Val Lys Pro